



SEQUENCE LISTING

110> Fryggvason, Karl
Salo, Sirpa

<120> Use of antibodies to the gamma 2 chain of laminin 5 to inhibit tumor growth and metastasis

<130> 02-1147

<150> 60/422,009

<151> 2002-10-29

<150> US 09/756,071

<151> 2001-01-08

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<170> PatentIn version 3.1

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Tyr	Arg	Val	Asp	Arg	Gly	Gly	Arg	His	Pro	Ser	Ala	His	Asp	Val	Ile	
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Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
515 520 525

Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
530 535 540

Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545 550 555 560

Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
565 570 575

Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
580 585 590

Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
595 600 605

Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
610 615 620

Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625 630 635 640

Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
645 650 655

Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
660 665 670

Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
675 680 685

Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
690 695 700

Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705 710 715 720

Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
725 730 735

Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
740 745 750

Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
755 760 765

Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
770 775 780

Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785 790 795 800

Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
805 810 815

Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
820 825 830

Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
835 840 845

Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
850 855 860

Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865 870 875 880

Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
885 890 895

Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
900 905 910

Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
915 920 925

Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
930 935 940

Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945 950 955 960

Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
965 970 975

Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
980 985 990

Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
995 1000 1005

Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
1010 1015 1020

Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly

1025		1030		1035
Ala Leu	Ala Met Glu Lys Gly	Leu Ala Ser Leu Lys	Ser Glu Met	
1040		1045	1050	
Arg Glu	Val Glu Gly Glu Leu	Glu Arg Lys Glu Leu	Glu Phe Asp	
1055		1060	1065	
Thr Asn	Met Asp Ala Val Gln	Met Val Ile Thr Glu	Ala Gln Lys	
1070		1075	1080	
Val Asp	Thr Arg Ala Lys Asn	Ala Gly Val Thr Ile	Gln Asp Thr	
1085		1090	1095	
Leu Asn	Thr Leu Asp Gly Leu	Leu His Leu Met Gly	Met	
1100		1105	1110	

<210> 5
 <211> 530
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Portion of Domain III of laminin gamma 2

<400> 5
 aattctgccca ggattgtgct tctggctaca agagagattc agcgagactg gggccttttg 60
 gcacctgtat tccttgtaac tgtcaagggg gaggggcctg tgatccagac acaggagatt 120
 gttattcagg ggatgagaat cctgacattg agtgtgctga ctgcccaatt ggtttctaca 180
 acgatccgca cgacccccgc agctgcaagc catgtccctg tcataacggg ttcagctgct 240
 cagtgattcc ggagacggag gaggtgggtg gcaataactg ccctcccggg gtcaccggtg 300
 cccgctgtga gctctgtgct gatggctact ttggggaccc ctttggtgaa catggcccag 360
 tgaggccttg tcagccctgt caatgcaaca gcaatgtgga cccagtgcc tctgggaatt 420
 gtgaccggct gacaggcagg tgtttgaagt gtatccacaa cacagccggc atctactgcg 480
 accagtgcaa agcaggctac ttcggggacc cattggctcc caaccagca 530

<210> 6
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>

<221> misc_feature

<223> Portion of Domain III of laminin gamma 2.

<400> 6

Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg
1 5 10 15

Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly
20 25 30

Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro
35 40 45

Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro His
50 55 60

Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys His Asn Gly Phe Ser Cys
65 70 75 80

Ser Val Met Pro Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Pro
85 90 95

Gly Val Thr Gly Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly
100 105 110

Asp Pro Phe Gly Glu His Gly Pro Val Arg Pro Cys Gln Pro Cys Gln
115 120 125

Cys Asn Asn Asn Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu
130 135 140

Thr Gly Arg Cys Leu Lys Cys Ile His Asn Thr Ala Gly Ile Tyr Cys
145 150 155 160

Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp Pro Leu Ala Pro Asn Pro
165 170 175

Ala

<210> 7

<211> 681
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Complete domain III of laminin gamma 2

<400> 7
tgtatatgtc ctgttgggta caaggggcaa ttctgccagg attgtgcttc tggctacaag 60
agagattcag cgagactggg gccttttggc acctgtattc cttgtaactg tcaaggggga 120
ggggcctgtg atccagacac aggagattgt tattcagggg atgagaatcc tgacattgag 180
tgtgctgact gcccaattgg tttctacaac gatccgcacg acccccgcag ctgcaagcca 240
tgtccctgtc ataacggggt cagctgctca gtgattccgg agacggagga ggtggtgtgc 300
aataactgcc ctcccggggt caccgggtgcc cgctgtgagc tctgtgctga tggctacttt 360
ggggaccctt ttggtgaaca tggcccagtg aggccttgtc agccctgtca atgcaacagc 420
aatgtggacc ccagtgcctc tgggaattgt gaccggctga caggcagggtg tttgaagtgt 480
atccacaaca cagccggcat ctactgcgac cagtgc aaag caggctactt cggggaccca 540
ttggctccca acccagcaga caagtgtcga gcttgcaact gtaaccccat gggctcagag 600
cctgtaggat gtcgaagtga tggcacctgt gtttgcaagc caggatttgg tggccccaac 660
tgtgagcatg gagcattcag c 681

<210> 8
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Complete domain III of laminin gamma 2.

<400> 8

Cys Ile Cys Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala
1 5 10 15
Ser Gly Tyr Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys
20 25 30
Ile Pro Cys Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly
35 40 45

Asp Cys Tyr Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys
50 55 60

Pro Ile Gly Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro
65 70 75 80

Cys Pro Cys His Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu
85 90 95

Glu Val Val Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys
100 105 110

Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly
115 120 125

Pro Val Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn Val Asp Pro
130 135 140

Ser Ala Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys
145 150 155 160

Ile His Asn Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr
165 170 175

Phe Gly Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys
180 185 190

Asn Cys Asn Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly
195 200 205

Thr Cys Val Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly
210 215 220

Ala Phe Ser
225

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature

<223> N-terminal portion of domain III of laminin gamma 2.

<400> 9

Cys Ile Cys Pro Val Gly Tyr Lys Gly
1 5

<210> 10

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> C-terminal portion of domain III of laminin gamma 2.

<400> 10

Asp Lys Cys Arg Ala Cys Asn Cys Asn Pro Met Gly Ser Glu Pro Val
1 5 10 15

Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe Gly Gly
20 25 30

Pro Asn Cys Glu His Gly Ala Phe Ser
35 40

1